



SEQUENCE LISTING

<110> Bowen, Benjamin A.
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Goldsmith, Neil
Haudenschild, Christian
Houck, David
McAlpine, James B.
Neilsen, Soren
Pazoles, Christopher
Spencer, Marget E.
Stafford, Angela

<120> Methods for Identifying Genes Regulating
Desired Cell Phenotypes

<130> 50273/005002

<140> US 10/056,479

<141> 2002-01-24

<150> US 60/263,807

<151> 2001-01-24

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

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His	Gly	Gly	Asn	Phe	Gln	Gly	Thr	Pro	Ile	Gly	Val	Ser	Met	Asp	Asn
			20					25					30		
Thr	Arg	Leu	Ala	Leu	Ala	Ala	Ile	Gly	Lys	Leu	Met	Phe	Ala	Gln	Phe
		35					40					45			
Ser	Glu	Leu	Val	Asn	Asp	Phe	Tyr	Asn	Asn	Gly	Leu	Pro	Ser	Asn	Leu
	50				55						60				
Ser	Gly	Ser	Arg	Asn	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Lys	Gly	Ala	Glu
65				70					75					80	
Ile	Ala	Met	Ala	Ser	Tyr	Cys	Ser	Glu	Leu	Gln	Phe	Leu	Gly	Asn	Pro
			85					90						95	
Val	Thr	Asn	His	Val	Gln	Ser	Ala	Glu	Gln	His	Asn	Gln	Asp	Val	Asn
		100					105						110		
Ser	Leu	Gly	Leu	Ile	Ser	Ser	Arg	Lys	Thr	Ala	Glu	Ala	Val	Asp	Ile
	115						120					125			
Leu	Lys	Leu	Met	Thr	Ser	Thr	Tyr	Leu	Val	Ala	Leu	Cys	Gln	Ala	Val
	130					135					140				
Asp	Leu	Arg	His	Met	Glu	Glu	Asn	Leu	Arg	Asn	Thr	Val	Lys	Asn	Thr
145					150				155						160

Val	Ser	Gln	Val	Ala	Lys	Arg	Thr	Leu	Thr	Thr	Gly	Ala	Asn	Gly	Glu
				165				170						175	
Leu	His	Pro	Ser	Arg	Phe	Cys	Glu	Lys	Asp	Leu	Leu	Lys	Val	Val	Asp
			180				185						190		
Arg	Glu	Tyr	Val	Phe	Ala	Tyr	Ile	Asp	Asp	Pro	Cys	Leu	Ala	Thr	Tyr
		195				200						205			
Pro	Leu	Met	Gln	Ser	Leu	Gly	Ala								
	210					215									

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<220>
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 gggaagctca tgtttgctca gttctccgag cttgtcaatg acttctacaa caatggctctg 180
 ccatcgaatc tgtctggcag caggaacccc agcttggact atgggcttaa aggagcggag 240
 atcgcaatgg cttctactg ttccgarctt cagttccttg gtaaccggt tactaaccat 300
 gtccagagcg ctgagcagca taaccaggat gtcaactcat tgggattgat ctcatcaagg 360
 aagacagctg aagctgttga catcttgaag ctcatgacat cgacttactt ggtggccctt 420
 tgccaagctg ttgacctgag gcacatggaa gagaatctta ggaacactgt gaagaacacc 480
 gtgagccaag tcgccaagag gacgctcacm acaggagcca acggtgagct tcacccatcg 540
 agattctgcg agaaggactt gctcaaagtr gttgacagag agtatgtgtt cgcgtacatt 600
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 <213> Artificial Sequence

<220>
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 1 5 10 15
 Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Tyr Ser Leu Val
 20 25 30
 Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Val Ile Leu Gly Ala
 35 40 45
 Asp Pro Leu Pro Glu Glu Lys Pro Met Phe Glu Leu Val Ser Ala Ala
 50 55 60
 Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala Ile Asp Gly His Leu Ser
 65 70 75 80
 Glu Val Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro Gly Leu Ile
 85 90 95
 Ser Lys Asn Ile Glu Lys Gly Leu Val Glu Ala Phe Lys Pro Ile Gly
 100 105 110
 Ile Glu Asp Gly Thr
 115

<210> 4

<211> 353
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> 183
<223> n = A,T,C or G

<223> Synthetic

<400> 4
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cgtggcccaa gcgataactca tttgtacagt cttgtaggtc aggccttggt cggagacgga 120
gctgcagcag tcattcctcgg agcagacccc cttcccgaag agaagcccat gtttgaactt 180
gtntctgcag ctccagaccat cttgccagac agtgaaggcg ccatcgacgg tcattcttagt 240
gaagttggtc tcacattcca tttgcttaag gacgttcccg ggctgatctc caagaacatt 300
gagaagggtc tagtcgagge attcaagcct atcggtatcg aagacggaac tca 353

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<221> VARIANT
<222> 52
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<223> Synthetic

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Pro Glu Ala Val Lys Asp Trp Arg Glu Ile Val Thr Tyr Phe Ser Tyr
1 5 10 15
Pro Val Ser Ala Arg Asp Tyr Ser Arg Trp Pro Asp Lys Pro Glu Ala
20 25 30
Trp Lys Glu Val Thr Lys Arg Tyr Ser Asp Thr Leu Met Gly Leu Ala
35 40 45
Cys Lys Leu Xaa Glu Val Leu Ser Glu Ala Met Gly Leu Glu Lys Glu
50 55 60
Ala Leu Thr Lys Ala Cys Val Asp Met Asp Gln Lys Val Val Val Asn
65 70 75 80
Tyr Tyr Pro Lys Cys Pro Glu Pro Asp Leu Thr Leu Gly Leu Lys Arg
85 90 95
His Thr Asp Pro Gly Thr Ile Thr Leu Leu Leu Gln Asp Gln Val Gly
100 105 110
Gly Leu Gln Ala Thr Arg Asp Asp Gly Lys
115 120

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<211> 368
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<220>
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<400> 6

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agcgacacgc tgatgggtct ggcatgtaag cttstaggagg tcttatctga agcgatggga 180
ctagagaagg aggctctgac taaggcctgt gttgacatgg accagaaagt tgttgtcaac 240
tactacccca agtgtcctga gcctgatcta actttgggac tcaagaggca taccgacccc 300
gggacgatca ccttgcttct ccaggaccaa gttggcgggc ttcaggccac tagagatgat 360
ggtaagac

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<211> 23
<212> DNA
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<220>
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<400> 7
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23

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<210> 8
<211> 22
<212> DNA
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<220>
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<400> 8
ggrtakatgt tytcraaggc rg

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22

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<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 9
atgatgtacc arcarggggtg cttygc

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26

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<210> 10
<211> 21
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<220>
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<400> 10
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21

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<210> 11
<211> 25
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<220>
<223> Synthetic

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